

PCT09

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/647,377

TIME: 15:05:38

Input Set : N:\COPIES\ES.txt

Output Set: N:\CRF3\11142001\I647377.raw

3 <110> APPLICANT: Rosenthal, Andre et al.

5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING PROTEINS WHICH INFLUENCE
BONE DEVELOPMENT

7 <130> FILE REFERENCE: 0147-0211P

9 <140> CURRENT APPLICATION NUMBER: 09/647,377

C--> 10 <141> CURRENT FILING DATE: 2000-09-24 *OK*

12 <160> NUMBER OF SEQ ID NOS: 34

14 <170> SOFTWARE: PatentIn version 3.1

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 1550

18 <212> TYPE: DNA

19 <213> ORGANISM: Mus musculus

21 <220> FEATURE:

22 <221> NAME/KEY: CDS

23 <222> LOCATION: (2)..(1180)

24 <223> OTHER INFORMATION:

27 <400> SEQUENCE: 1

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 29 Leu Gly Arg Ser Lys Val Ala Ala Glu Arg Ala Thr Ser Val Tyr Leu
 30 1 5 10 15
 32 gtc cag aag gtg gtc ccc atg ctt ccc agg ctt ctg tgt gag gaa ctc 97
 33 Val Gln Lys Val Val Pro Met Leu Pro Arg Leu Leu Cys Glu Glu Leu
 34 20 25 30
 36 tgc agc ctc aac ccc atg act gac aag ctg acc ttc tct gtg atc tgg 145
 37 Cys Ser Leu Asn Pro Met Thr Asp Lys Leu Thr Phe Ser Val Ile Trp
 38 35 40 45
 40 aag ctg acc cct gaa ggc aag atc ctt gaa gag tgg ttt ggc cgc act 193
 41 Lys Leu Thr Pro Glu Gly Lys Ile Leu Glu Glu Trp Phe Gly Arg Thr
 42 50 55 60
 44 atc atc cgt tct tgc acc aaa ctg agc tac gac cat gcc cag agc atg 241
 45 Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr Asp His Ala Gln Ser Met
 46 65 70 75 80
 48 atc gaa aat cca act gag aag atc cct gag gaa gag ctt ccc cca att 289
 49 Ile Glu Asn Pro Thr Glu Lys Ile Pro Glu Glu Glu Leu Pro Pro Ile
 50 85 90 95
 52 tct cca gag cac agc gtc gag gag gtg cac cag gca gtc ctg aac ctg 337
 53 Ser Pro Glu His Ser Val Glu Glu Val His Gln Ala Val Leu Asn Leu
 54 100 105 110
 56 cac agc att gca aag caa ctc cgc cgc cag cgc ttt gta gat ggc gca 385
 57 His Ser Ile Ala Lys Gln Leu Arg Arg Gln Arg Phe Val Asp Gly Ala
 58 115 120 125
 60 ctc cgt tta gat cag gag ttc atg ctc ctg gcc aac atg gcg gtg gcc 433
 61 Leu Arg Leu Asp Gln Glu Phe Met Leu Leu Ala Asn Met Ala Val Ala
 62 130 135 140
 64 cac aag atc ttc cgc acc ttc cct gag cag gcc ctg ctg cgc cgg cat 481
 65 His Lys Ile Phe Arg Thr Phe Pro Glu Gln Ala Leu Leu Arg Arg His
 66 145 150 155 160
 68 ccc cca cca cag acg aag atg ctc agt gac ctg gtg gag ttc tgt gac 529

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69 Pro Pro Pro Gln Thr Lys Met Leu Ser Asp Leu Val Glu Phe Cys Asp
70          165          170          175
72 cag atg ggg ctg ccc atg gat gtc agc tct gca ggg gcc cta aat atg      577
73 Gln Met Gly Leu Pro Met Asp Val Ser Ser Ala Gly Ala Leu Asn Met
74          180          185          190
76 gca ctg tac ttc tgc tct ggg atg ctg cag gac cag gag cag ttc cgg      625
77 Ala Leu Tyr Phe Cys Ser Gly Met Leu Gln Asp Gln Glu Gln Phe Arg
78          195          200          205
80 cat tat gct ctc aac gtt ccc ctc tac aca cac ttc acc tct ccc atc      673
81 His Tyr Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile
82          210          215          220
84 cgc cgc ttt gct gac gtc ata gtg cac cgc ctc ctg gct gct gct ctg      721
85 Arg Arg Phe Ala Asp Val Ile Val His Arg Leu Leu Ala Ala Ala Leu
86 225          230          235          240
88 ggc tac agt gaa cag cca gat gtg gag cct gat acc cta cag aag caa      769
89 Gly Tyr Ser Glu Gln Pro Asp Val Glu Pro Asp Thr Leu Gln Lys Gln
90          245          250          255
92 gct gac cac tgc aat gac cgt cgc atg gct tcc aaa cgt gtg cag gag      817
93 Ala Asp His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu
94          260          265          270
96 ctc agc atc ggc ctc ttc ttc gca gtt cta gta aag gag agt ggc ccc      865
97 Leu Ser Ile Gly Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro
98          275          280          285
100 ctg gag tcc gaa gcc atg gtg atg ggt gtc ctg aac caa gct ttc gac      913
101 Leu Glu Ser Glu Ala Met Val Met Gly Val Leu Asn Gln Ala Phe Asp
102          290          295          300
104 gtg ctg gtg ctg cgc ttt ggg gtg cag aag cgc atc tac tgc aat gca      961
105 Val Leu Val Leu Arg Phe Gly Val Gln Lys Arg Ile Tyr Cys Asn Ala
106 305          310          315          320
108 ctg gcc ctg cga tcc tac agc ttc cag aag gtg ggg aag aag cca gag      1009
109 Leu Ala Leu Arg Ser Tyr Ser Phe Gln Lys Val Gly Lys Lys Pro Glu
110          325          330          335
112 ctc act ctt gtt tgg gag cct gat gac ctt gaa gag gag cca aca cag      1057
113 Leu Thr Leu Val Trp Glu Pro Asp Asp Leu Glu Glu Glu Pro Thr Gln
114          340          345          350
116 cag gtc atc acc atc ttc agc ctg gtg gat gtg gtc ctg cag gca gag      1105
117 Gln Val Ile Thr Ile Phe Ser Leu Val Asp Val Val Leu Gln Ala Glu
118          355          360          365
120 gcc aca gcc ctc aag tac agt gct atc ctg aag cga cca ggc ctg gag      1153
121 Ala Thr Ala Leu Lys Tyr Ser Ala Ile Leu Lys Arg Pro Gly Leu Glu
122          370          375          380
124 aag gcg tct gat gag gag cct gag gac tgaatgctag cccaagccag      1200
125 Lys Ala Ser Asp Glu Glu Pro Glu Asp
126 385          390
128 gcctgtgcct gccctaccct gctggctttt aggaatagga ccttttgaca ccaaagggga      1260
130 tttttaattt ggtttttaac aactcagggg ttgttttta tttttatttt tccttttatt      1320
132 ttacttttgc agctcagttt ttaaataaac tggaagggtta ggggtcaggg caggggatgc      1380
134 tgaggcctgg cctgtgcttc cctgagcaga gaggatecca gtcctcctgg gcaggcagcc      1440
136 ccgctttctac caggcgaccc actgcccttc cctgcccagg aaatgggggg tttcagcaaa      1500

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138 tcagtgtcat ggaataaaat caagtgtgaa ttgcaaaaaa aaaaaaaaaa 1550
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 393
143 <212> TYPE: PRT
144 <213> ORGANISM: Mus musculus
146 <400> SEQUENCE: 2
148 Leu Gly Arg Ser Lys Val Ala Ala Glu Arg Ala Thr Ser Val Tyr Leu
149 1 5 10 15
152 Val Gln Lys Val Val Pro Met Leu Pro Arg Leu Leu Cys Glu Glu Leu
153 20 25 30
156 Cys Ser Leu Asn Pro Met Thr Asp Lys Leu Thr Phe Ser Val Ile Trp
157 35 40 45
160 Lys Leu Thr Pro Glu Gly Lys Ile Leu Glu Glu Trp Phe Gly Arg Thr
161 50 55 60
164 Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr Asp His Ala Gln Ser Met
165 65 70 75 80
168 Ile Glu Asn Pro Thr Glu Lys Ile Pro Glu Glu Glu Leu Pro Pro Ile
169 85 90 95
172 Ser Pro Glu His Ser Val Glu Glu Val His Gln Ala Val Leu Asn Leu
173 100 105 110
176 His Ser Ile Ala Lys Gln Leu Arg Arg Gln Arg Phe Val Asp Gly Ala
177 115 120 125
180 Leu Arg Leu Asp Gln Glu Phe Met Leu Leu Ala Asn Met Ala Val Ala
181 130 135 140
184 His Lys Ile Phe Arg Thr Phe Pro Glu Gln Ala Leu Leu Arg Arg His
185 145 150 155 160
188 Pro Pro Pro Gln Thr Lys Met Leu Ser Asp Leu Val Glu Phe Cys Asp
189 165 170 175
192 Gln Met Gly Leu Pro Met Asp Val Ser Ser Ala Gly Ala Leu Asn Met
193 180 185 190
196 Ala Leu Tyr Phe Cys Ser Gly Met Leu Gln Asp Gln Glu Gln Phe Arg
197 195 200 205
200 His Tyr Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile
201 210 215 220
204 Arg Arg Phe Ala Asp Val Ile Val His Arg Leu Leu Ala Ala Ala Leu
205 225 230 235 240
208 Gly Tyr Ser Glu Gln Pro Asp Val Glu Pro Asp Thr Leu Gln Lys Gln
209 245 250 255
212 Ala Asp His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu
213 260 265 270
216 Leu Ser Ile Gly Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro
217 275 280 285
220 Leu Glu Ser Glu Ala Met Val Met Gly Val Leu Asn Gln Ala Phe Asp
221 290 295 300
224 Val Leu Val Leu Arg Phe Gly Val Gln Lys Arg Ile Tyr Cys Asn Ala
225 305 310 315 320
228 Leu Ala Leu Arg Ser Tyr Ser Phe Gln Lys Val Gly Lys Lys Pro Glu
229 325 330 335
232 Leu Thr Leu Val Trp Glu Pro Asp Asp Leu Glu Glu Glu Pro Thr Gln

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233          340          345          350
236 Gln Val Ile Thr Ile Phe Ser Leu Val Asp Val Val Leu Gln Ala Glu
237          355          360          365
240 Ala Thr Ala Leu Lys Tyr Ser Ala Ile Leu Lys Arg Pro Gly Leu Glu
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244 Lys Ala Ser Asp Glu Glu Pro Glu Asp
245 385          390
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1140
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (2)..(781)
256 <223> OTHER INFORMATION:
259 <400> SEQUENCE: 3
260 g atc cac cgc gcc ttc ccc gag cag gcc ctg ctg cgc cgg cac ccc ccg      49
261   ile His Arg Ala Phe Pro.Glu Gln Ala Leu Leu Arg Arg His Pro Pro
262   1          5          10          15
264 ccc caa aca agg atg ctc agt gac ctg gtg gaa ttc tgc gac cag atg      97
265 Pro Gln Thr Arg Met Leu Ser Asp Leu Val Glu Phe Cys Asp Gln Met
266          20          25          30
268 ggg ctg ccc gtg gac ttc agc tcc gca gga gcc ctc aat atg gca ctg      145
269 Gly Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn Met Ala Leu
270          35          40          45
272 tac ttc tgc tcg ggg ctg ctg cag gac cca gcg cag ttc cgg cac tac      193
273 Tyr Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr
274          50          55          60
276 gcg ctc aat gtg ccc ctg tac aca cac ttc acc tcg ccc atc cgc cgc      241
277 Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile Arg Arg
278 65          70          75          80
280 ttt gcc gac gtc ctg gtg cac cgc ctc ctg gct gcc gcg tta ggc tat      289
281 Phe Ala Asp Val Leu Val His Arg Leu Leu Ala Ala Ala Leu Gly Tyr
282          85          90          95
284 agg gag cga cta gac atg gcg ccc gat acc ctg cag aaa cag gcg gac      337
285 Arg Glu Arg Leu Asp Met Ala Pro Asp Thr Leu Gln Lys Gln Ala Asp
286          100          105          110
288 cac tgt aac gac cgc cgc atg gcg tcc aag cgc gtg cag gag ctc agt      385
289 His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu Leu Ser
290          115          120          125
292 acc agt ctc ttc ttt gct gtt ctg gtc aag gag agt ggc ccc ctg gag      433
293 Thr Ser Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro Leu Glu
294          130          135          140
296 tca gaa gcc atg gtg atg ggc atc ctg aag caa gcc ttc gac gtg ctg      481
297 Ser Glu Ala Met Val Met Gly Ile Leu Lys Gln Ala Phe Asp Val Leu
298 145          150          155          160
300 gtg ctg cgc tac ggc gtg cag aag cgc atc tac tgc aac gca ctg gcc      529
301 Val Leu Arg Tyr Gly Val Gln Lys Arg Ile Tyr Cys Asn Ala Leu Ala
302          165          170          175

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304 ctg cgg tcc cac cac ttc cag aag gtg ggc aag aag ccg gaa ctc acg      577
305 Leu Arg Ser His His Phe Gln Lys Val Gly Lys Lys Pro Glu Leu Thr
306          180          185          190
308 ctg gtc tgg gag cct gag gac atg gag cag gag cca gca cag cag gtc      625
309 Leu Val Trp Glu Pro Glu Asp Met Glu Gln Glu Pro Ala Gln Gln Val
310          195          200          205
312 atc acc atc ttc agc ctg gtg gag gtg gtc ctg cag gca gag tcc aca      673
313 Ile Thr Ile Phe Ser Leu Val Glu Val Val Leu Gln Ala Glu Ser Thr
314          210          215          220
316 gcc ctc aag tac agc gcc atc ctg aag cgg cca ggc acc cag ggc cac      721
317 Ala Leu Lys Tyr Ser Ala Ile Leu Lys Arg Pro Gly Thr Gln Gly His
318 225          230          235          240
320 ctg ggc cct gag aag gag gag gag gag tct gac ggt gag ccc gag gac      769
321 Leu Gly Pro Glu Lys Glu Glu Glu Glu Ser Asp Gly Glu Pro Glu Asp
322          245          250          255
324 tca agc acc agc tgagctccac cagccgctg ccccgctgc cccgctgcc      821
325 Ser Ser Thr Ser
326          260
328 tgtcccgcca cactggcttt aggacctgtt gacacggagg ggggttttta atttggtttt      881
330 taacaactca ggggtttgtt tttattttta ttttaatttt gcagctcaac ttttaaacia      941
332 actgcagggg agaggggtggg gctggaagga aggctgaggc ctggtcagca gtgaccccag      1001
334 cagagcaggc cccagtcctc ctgggaggct ggccccctt ttttctgggc cctactgcc      1061
336 tcctctgccc aggaaatggg ggggtttcag caactcagtg tcacagaata aaatcaagtg      1121
338 tggagtgcc taaaaaaaaa
341 <210> SEQ ID NO: 4
342 <211> LENGTH: 260
343 <212> TYPE: PRT
344 <213> ORGANISM: Homo sapiens
346 <400> SEQUENCE: 4
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352 Pro Gln Thr Arg Met Leu Ser Asp Leu Val Glu Phe Cys Asp Gln Met
353          20          25          30
356 Gly Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn Met Ala Leu
357          35          40          45
360 Tyr Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr
361          50          55          60
364 Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile Arg Arg
365 65          70          75          80
368 Phe Ala Asp Val Leu Val His Arg Leu Leu Ala Ala Ala Leu Gly Tyr
369          85          90          95
372 Arg Glu Arg Leu Asp Met Ala Pro Asp Thr Leu Gln Lys Gln Ala Asp
373          100          105          110
376 His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu Leu Ser
377          115          120          125
380 Thr Ser Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro Leu Glu
381          130          135          140
384 Ser Glu Ala Met Val Met Gly Ile Leu Lys Gln Ala Phe Asp Val Leu
385 145          150          155          160

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : N:\COPIES\ES.txt

Output Set: N:\CRF3\11142001\I647377.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:19661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

L:19665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

L:19685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:19689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23